



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:28 PM GMT

PDB ID : 4UHX  
Title : Human aldehyde oxidase in complex with phthalazine and thioridazine  
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Deposited on : 2015-03-26  
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20026982

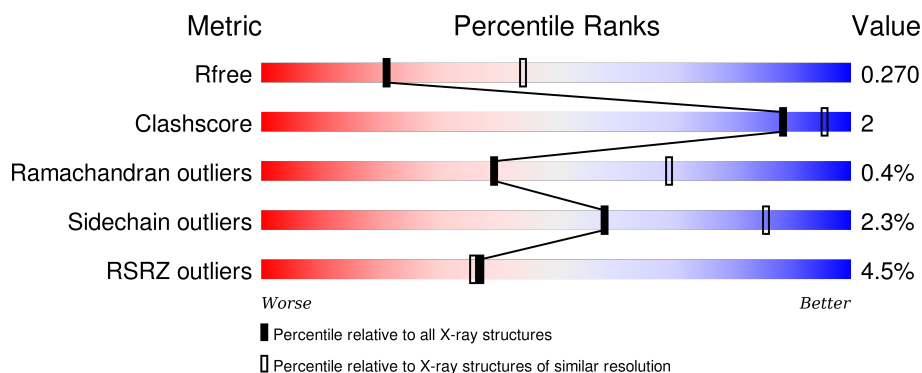
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1338	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	4FT	A	3007	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
9	MLI	A	3010	-	-	-	X
9	MLI	A	3011	-	-	-	X

## 2 Entry composition [i](#)

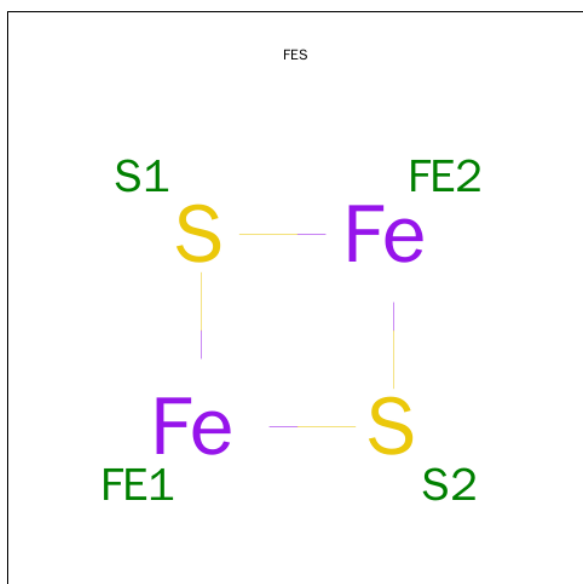
There are 10 unique types of molecules in this entry. The entry contains 10223 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called ALDEHYDE OXIDASE.

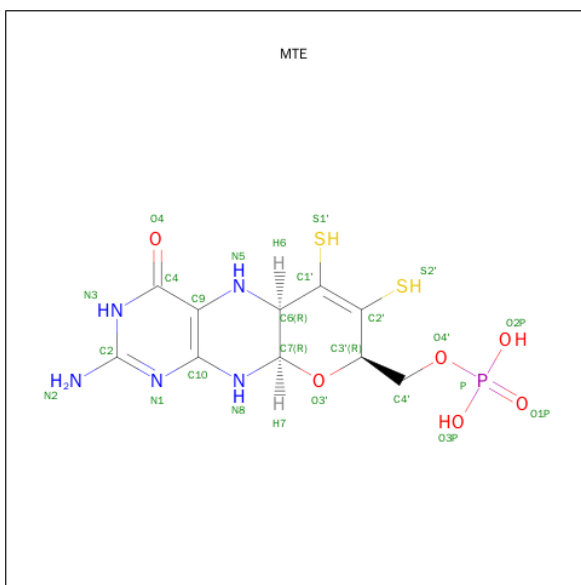
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1290	Total	C	N	O	S	0	0	0
			10000	6356	1724	1840	80			

- Molecule 2 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe<sub>2</sub>S<sub>2</sub>).



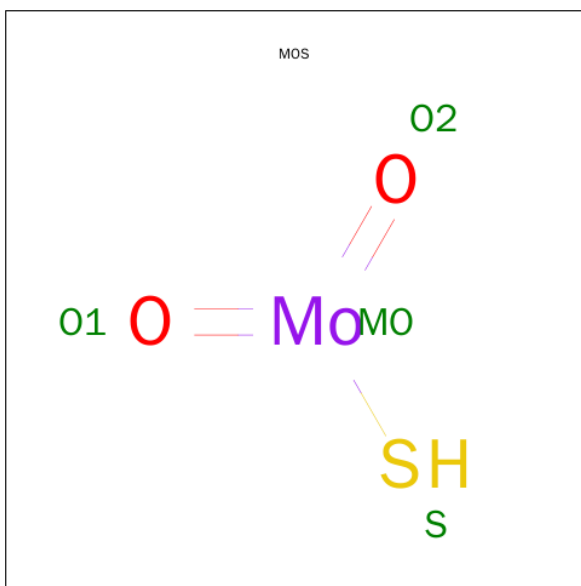
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	Fe	S	0	0
			4	2	2		
2	A	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 3 is PHOSPHONIC ACIDMONO-(2-AMINO-5,6-DIMERCAPTO-4-OXO-3,7,8A, 9,10,10A-HEXAHYDRO-4H-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-7-YLMETHYL) ESTER (three-letter code: MTE) (formula: C<sub>10</sub>H<sub>14</sub>N<sub>5</sub>O<sub>6</sub>PS<sub>2</sub>).



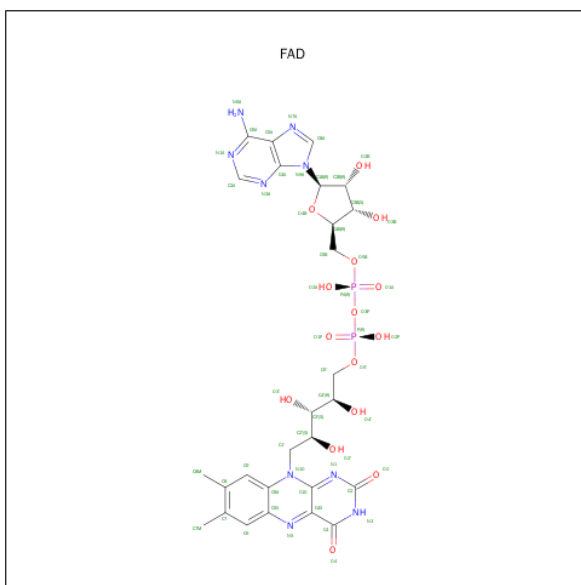
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			24	10	5	6	1	2		

- Molecule 4 is DIOXOTHIOMOLYBDENUM(VI) ION (three-letter code: MOS) (formula:  $\text{HMoO}_2\text{S}$ ).



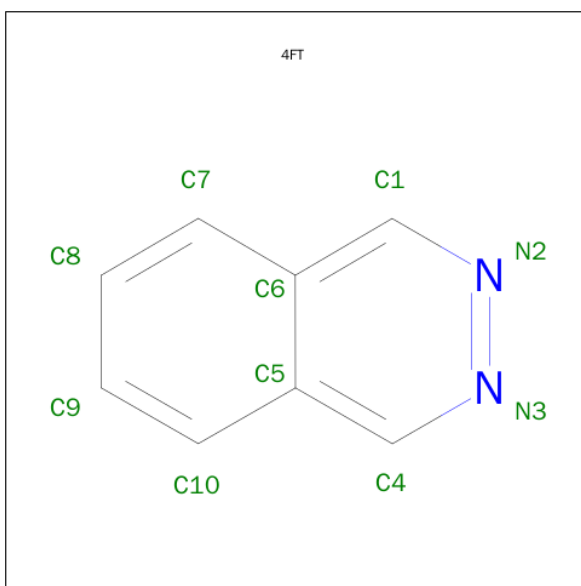
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	Mo	O	S	0	0
			4	1	2	1		

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $\text{C}_{27}\text{H}_{33}\text{N}_9\text{O}_{15}\text{P}_2$ ).



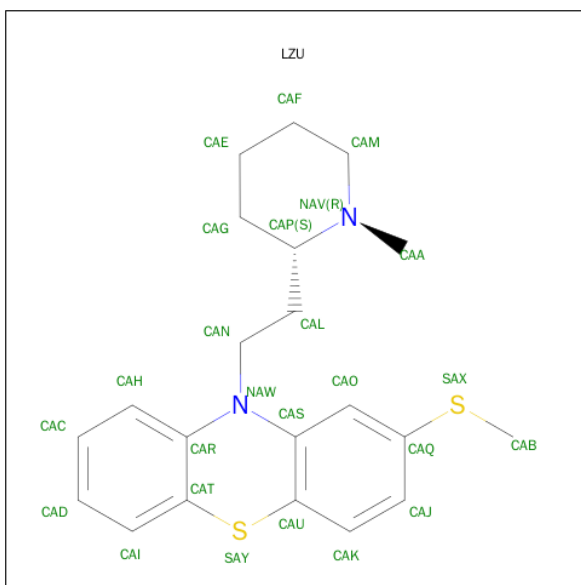
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 6 is PHTHALAZINE (three-letter code: 4FT) (formula:  $C_8H_6N_2$ ).



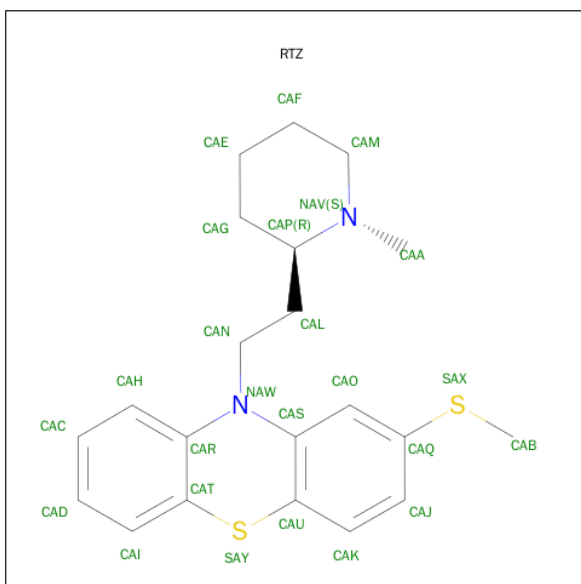
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N	0	0
			10	8	2		

- Molecule 7 is 10-{2-[(2S)-1-METHYLPYPERIDIN-2-YL]ETHYL}-2-(METHYLSULFANYL)-10H-PHENOTHIAZINE (three-letter code: LZU) (formula:  $C_{21}H_{26}N_2S_2$ ).



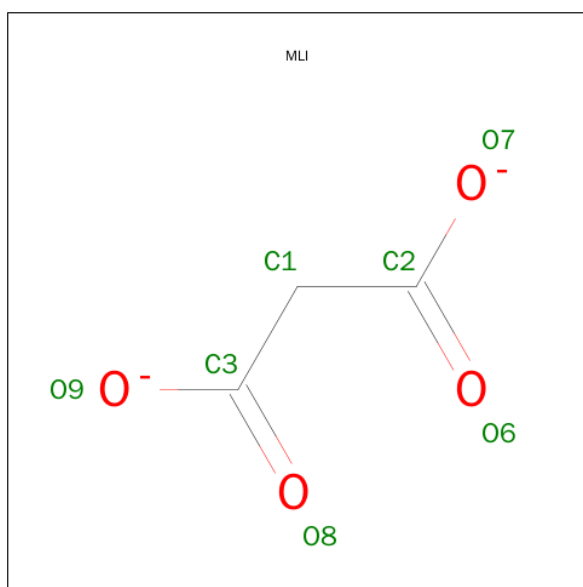
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	S	0	1
			25	21	2	2		

- Molecule 8 is 10-{2-[(2R)-1-METHYLPIPERIDIN-2-YL]ETHYL}-2-(METHYLSULFANYL)-10H-PHENOTHIAZINE (three-letter code: RTZ) (formula:  $C_{21}H_{26}N_2S_2$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	S	0	1
			25	21	2	2		

- Molecule 9 is MALONATE ION (three-letter code: MLI) (formula:  $C_3H_2O_4$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			7	3	4		
9	A	1	Total	C	O	0	0
			7	3	4		

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	60	Total	O	0	0
			60	60		



### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: ALDEHYDE OXIDASE



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	148.73Å 148.73Å 132.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	105.17 – 2.70 40.80 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.8 (105.17-2.70) 99.8 (40.80-2.70)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.30 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, $R_{free}$	0.195 , 0.244 0.232 , 0.270	Depositor DCC
$R_{free}$ test set	2085 reflections (5.30%)	DCC
Wilson B-factor (Å <sup>2</sup> )	69.0	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 38.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 41407 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	10223	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MOS, MLI, LZU, FES, 4FT, MTE, FAD, RTZ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.36	0/10210	0.58	0/13805

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10000	0	10065	44	0
2	A	8	0	0	0	0
3	A	24	0	10	0	0
4	A	4	0	0	1	0
5	A	53	0	31	0	0
6	A	10	0	6	0	0
7	A	25	0	26	2	0
8	A	25	0	26	3	0
9	A	14	0	4	0	0
10	A	60	0	0	0	0
All	All	10223	0	10168	50	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (50) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:3009[B]:RTZ:CAH	8:A:3009[B]:RTZ:HALA	1.92	0.95
1:A:449:PHE:CE1	1:A:456:ILE:HG22	2.02	0.95
1:A:453:ASP:OD1	1:A:454:GLY:N	1.98	0.95
1:A:450:GLY:O	1:A:452:GLY:N	2.01	0.92
8:A:3009[B]:RTZ:HAH	8:A:3009[B]:RTZ:HALA	1.55	0.88
1:A:449:PHE:HE1	1:A:456:ILE:HG22	1.39	0.84
7:A:3008[A]:LZU:CAH	7:A:3008[A]:LZU:H20	2.19	0.71
8:A:3009[B]:RTZ:CAH	8:A:3009[B]:RTZ:CAL	2.69	0.68
4:A:3004:MOS:MO	4:A:3004:MOS:O2	1.72	0.60
1:A:379:LEU:HD21	1:A:392:LEU:HD12	1.86	0.58
1:A:466:VAL:HG11	1:A:519:ILE:HD11	1.85	0.58
1:A:453:ASP:CG	1:A:454:GLY:N	2.57	0.58
7:A:3008[A]:LZU:CAH	7:A:3008[A]:LZU:CAL	2.78	0.58
1:A:1185:THR:HG21	1:A:1208:PHE:CZ	2.40	0.56
1:A:870:MET:SD	1:A:931:ILE:HD13	2.46	0.55
1:A:433:ARG:NH1	1:A:1238:ILE:O	2.41	0.54
1:A:323:VAL:HG12	1:A:331:THR:HB	1.90	0.52
1:A:1191:VAL:HG23	1:A:1268:LEU:CD2	2.40	0.52
1:A:55:MET:CE	1:A:127:THR:HA	2.40	0.51
1:A:111:GLY:HA2	1:A:156:PRO:HB2	1.93	0.51
1:A:332:GLN:HG3	1:A:425:VAL:HG23	1.93	0.51
1:A:471:ILE:HD12	1:A:501:VAL:HG12	1.93	0.50
1:A:613:THR:HG22	1:A:686:ALA:HB1	1.93	0.50
1:A:501:VAL:O	1:A:501:VAL:HG23	2.13	0.48
1:A:578:ASP:OD2	1:A:1061:ARG:NH1	2.47	0.47
1:A:447:VAL:HG12	1:A:459:LEU:CD1	2.44	0.47
1:A:447:VAL:HG13	1:A:526:PHE:CZ	2.50	0.46
1:A:921:ARG:NE	1:A:1269:GLY:O	2.46	0.46
1:A:211:ASP:OD1	1:A:213:THR:HG22	2.15	0.46
1:A:1191:VAL:HG22	1:A:1191:VAL:O	2.14	0.46
1:A:233:THR:HG21	1:A:255:PHE:CE2	2.51	0.45
1:A:893:LYS:HG2	1:A:1015:PRO:HG2	1.99	0.45
1:A:570:ILE:HD11	1:A:573:LYS:HE3	1.98	0.45
1:A:625:VAL:HG23	1:A:696:VAL:HG23	1.98	0.45
1:A:55:MET:HE1	1:A:130:ARG:HG3	1.99	0.45
1:A:1012:LEU:HB2	1:A:1275:LEU:HD21	1.98	0.44
1:A:629:LEU:HD22	1:A:641:ILE:HG21	1.99	0.44
1:A:128:LEU:HD22	1:A:140:LEU:HA	1.99	0.44
1:A:587:LEU:HD11	1:A:1056:ILE:HG13	2.00	0.43
1:A:931:ILE:HD12	1:A:932:THR:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:490:LEU:HD11	1:A:527:TYR:CG	2.55	0.42
1:A:450:GLY:C	1:A:452:GLY:N	2.73	0.42
1:A:28:LEU:HB3	1:A:29:PRO:HD3	2.02	0.42
1:A:388:ARG:NH1	1:A:409:GLU:OE2	2.53	0.41
1:A:449:PHE:O	1:A:457:ARG:HD2	2.20	0.41
1:A:625:VAL:CG2	1:A:696:VAL:HG23	2.50	0.41
1:A:735:VAL:HA	1:A:860:MET:CE	2.51	0.41
1:A:556:LEU:HD11	1:A:1003:LYS:HE3	2.03	0.41
1:A:779:LYS:NZ	1:A:783:ASP:OD2	2.53	0.41
1:A:1062:GLU:O	1:A:1107:LEU:HD11	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	1278/1338 (96%)	1237 (97%)	36 (3%)	5 (0%)	39 69

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	451	GLU
1	A	1257	GLN
1	A	532	GLN
1	A	921	ARG
1	A	811	VAL

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar

resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	1094/1136 (96%)	1069 (98%)	25 (2%)	58 85

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	CYS
1	A	88	THR
1	A	114	CYS
1	A	208	LEU
1	A	277	PHE
1	A	304	LEU
1	A	325	LYS
1	A	338	LEU
1	A	425	VAL
1	A	496	LEU
1	A	544	SER
1	A	568	GLN
1	A	654	CYS
1	A	701	GLU
1	A	712	GLN
1	A	751	PHE
1	A	752	TYR
1	A	777	PHE
1	A	845	THR
1	A	856	LYS
1	A	880	LEU
1	A	1268	LEU
1	A	1301	THR
1	A	1312	ARG
1	A	1336	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	147	ASN
1	A	231	GLN
1	A	568	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

10 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	FES	A	3001	1	0,4,4	0.00	-	0,4,4	0.00	-
2	FES	A	3002	1	0,4,4	0.00	-	0,4,4	0.00	-
3	MTE	A	3003	4	21,26,26	1.55	2 (9%)	18,40,40	2.01	6 (33%)
4	MOS	A	3004	3	0,3,3	0.00	-	0,3,3	0.00	-
5	FAD	A	3006	-	52,58,58	1.51	7 (13%)	52,89,89	2.17	10 (19%)
6	4FT	A	3007	-	11,11,11	1.29	0	14,14,14	1.43	2 (14%)
7	LZU	A	3008[A]	-	28,28,28	1.57	4 (14%)	35,39,39	1.31	4 (11%)
8	RTZ	A	3009[B]	-	28,28,28	1.59	5 (17%)	35,39,39	1.30	6 (17%)
9	MLI	A	3010	-	0,6,6	0.00	-	0,7,7	0.00	-
9	MLI	A	3011	-	0,6,6	0.00	-	0,7,7	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	FES	A	3001	1	-	0/0/4/4	0/1/1/1
2	FES	A	3002	1	-	0/0/4/4	0/1/1/1
3	MTE	A	3003	4	-	0/6/34/34	0/3/3/3
4	MOS	A	3004	3	-	0/0/0/0	0/0/0/0
5	FAD	A	3006	-	-	0/30/50/50	0/6/6/6
6	4FT	A	3007	-	-	0/0/0/0	0/2/2/2
7	LZU	A	3008[A]	-	-	0/7/30/30	0/4/4/4
8	RTZ	A	3009[B]	-	-	0/7/30/30	0/4/4/4
9	MLI	A	3010	-	-	0/0/4/4	0/0/0/0
9	MLI	A	3011	-	-	0/0/4/4	0/0/0/0

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	3008[A]	LZU	CAT-SAY	-5.51	1.66	1.76
8	A	3009[B]	RTZ	CAT-SAY	-5.34	1.66	1.76
8	A	3009[B]	RTZ	CAS-NAW	-3.43	1.35	1.40
7	A	3008[A]	LZU	CAR-NAW	-3.22	1.35	1.40
7	A	3008[A]	LZU	CAS-NAW	-3.20	1.35	1.40
8	A	3009[B]	RTZ	CAR-NAW	-3.13	1.35	1.40
7	A	3008[A]	LZU	CAU-SAY	-2.91	1.70	1.76
8	A	3009[B]	RTZ	CAU-SAY	-2.84	1.71	1.76
8	A	3009[B]	RTZ	CAG-CAP	2.19	1.57	1.52
5	A	3006	FAD	C10-N10	2.75	1.42	1.39
5	A	3006	FAD	C5A-C4A	3.29	1.47	1.40
5	A	3006	FAD	C9A-N10	3.37	1.43	1.38
5	A	3006	FAD	C8-C7	3.45	1.50	1.41
5	A	3006	FAD	C4-C4X	3.77	1.48	1.41
3	A	3003	MTE	C9-C10	3.88	1.48	1.41
5	A	3006	FAD	C9A-C5X	3.96	1.50	1.42
5	A	3006	FAD	C4X-C10	4.52	1.49	1.40
3	A	3003	MTE	C4-C9	5.06	1.48	1.41

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	3006	FAD	N3A-C2A-N1A	-7.81	122.73	128.87
7	A	3008[A]	LZU	CAM-NAV-CAP	-5.57	102.34	112.86
5	A	3006	FAD	C4-C4X-C10	-4.23	117.23	119.94
8	A	3009[B]	RTZ	CAE-CAF-CAM	-4.08	102.90	111.22
5	A	3006	FAD	C4X-C4-N3	-4.06	118.22	123.52
6	A	3007	4FT	C5-C4-N3	-3.48	120.60	124.45
6	A	3007	4FT	C6-C1-N2	-3.44	120.64	124.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	3006	FAD	N3-C2-N1	-3.05	122.56	127.69
8	A	3009[B]	RTZ	CAM-NAV-CAP	-2.86	107.45	112.86
8	A	3009[B]	RTZ	CAF-CAM-NAV	-2.72	106.49	111.06
8	A	3009[B]	RTZ	CAL-CAP-CAG	-2.40	109.09	112.32
8	A	3009[B]	RTZ	CAF-CAE-CAG	-2.15	106.99	111.44
3	A	3003	MTE	O3'-C7-C6	-2.12	107.51	108.96
5	A	3006	FAD	C1B-N9A-C4A	-2.04	124.53	126.81
7	A	3008[A]	LZU	CAG-CAP-NAV	-2.03	106.43	111.11
5	A	3006	FAD	C2A-N1A-C6A	2.01	122.36	118.77
7	A	3008[A]	LZU	CAB-SAX-CAQ	2.02	108.72	103.36
3	A	3003	MTE	O3P-P-O2P	2.06	115.02	107.44
8	A	3009[B]	RTZ	CAB-SAX-CAQ	2.11	108.96	103.36
7	A	3008[A]	LZU	CAN-NAW-CAS	2.19	122.08	118.99
3	A	3003	MTE	C4-C9-C10	2.40	116.72	114.61
5	A	3006	FAD	C4-C4X-N5	2.52	121.76	118.70
3	A	3003	MTE	C2-N1-C10	2.91	121.16	114.63
3	A	3003	MTE	N8-C10-N1	3.35	121.96	116.62
5	A	3006	FAD	C1'-N10-C9A	3.65	123.07	118.83
5	A	3006	FAD	C4X-N5-C5X	3.89	121.31	116.72
3	A	3003	MTE	C4-N3-C2	5.30	122.09	115.88
5	A	3006	FAD	C4-N3-C2	8.58	122.32	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	3004	MOS	1	0
7	A	3008[A]	LZU	2	0
8	A	3009[B]	RTZ	3	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	1290/1338 (96%)	0.34	58 (4%) 37 36	48, 76, 106, 134	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	557	HIS	5.2
1	A	572	PRO	4.1
1	A	731	ALA	4.1
1	A	967	GLU	4.0
1	A	167	THR	4.0
1	A	734	VAL	3.9
1	A	738	ILE	3.7
1	A	732	PHE	3.6
1	A	4	ALA	3.6
1	A	8	LEU	3.5
1	A	208	LEU	3.4
1	A	1271	SER	3.3
1	A	1328	PRO	3.3
1	A	868	LEU	3.3
1	A	1296	LEU	3.3
1	A	301	TYR	3.3
1	A	229	GLN	3.3
1	A	1299	PRO	3.3
1	A	560	HIS	3.2
1	A	623	LYS	3.1
1	A	549	TYR	3.0
1	A	213	THR	3.0
1	A	625	VAL	2.9
1	A	62	ILE	2.9
1	A	166	LYS	2.8
1	A	558	SER	2.7
1	A	280	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	1157	GLN	2.7
1	A	624	ILE	2.7
1	A	164	PHE	2.6
1	A	698	GLN	2.6
1	A	279	GLY	2.6
1	A	44	CYS	2.6
1	A	878	ALA	2.6
1	A	1207	ALA	2.6
1	A	1297	HIS	2.5
1	A	19	LYS	2.5
1	A	703	LEU	2.4
1	A	859	PHE	2.4
1	A	562	CYS	2.3
1	A	1300	LEU	2.3
1	A	1268	LEU	2.3
1	A	224	ILE	2.3
1	A	165	CYS	2.2
1	A	922	GLY	2.2
1	A	697	TYR	2.2
1	A	571	GLY	2.2
1	A	1113	ILE	2.2
1	A	1211	GLY	2.2
1	A	545	LEU	2.1
1	A	20	ASN	2.1
1	A	1120	GLY	2.1
1	A	885	PHE	2.1
1	A	547	ASP	2.0
1	A	733	LYS	2.0
1	A	231	GLN	2.0
1	A	716	SER	2.0
1	A	728	VAL	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
9	MLI	A	3011	7/7	0.84	0.55	7.60	67,68,69,71	7
9	MLI	A	3010	7/7	0.80	0.38	6.99	62,64,64,64	7
6	4FT	A	3007	10/10	0.75	0.43	4.01	102,102,103,103	0
8	RTZ	A	3009[B]	25/25	0.94	0.20	0.16	74,84,88,89	25
7	LZU	A	3008[A]	25/25	0.93	0.19	0.07	80,92,98,100	25
5	FAD	A	3006	53/53	0.94	0.19	-0.19	55,60,67,68	0
2	FES	A	3001	4/4	0.95	0.18	-1.16	47,49,49,52	0
3	MTE	A	3003	24/24	0.89	0.19	-1.58	79,85,87,89	0
4	MOS	A	3004	4/4	0.93	0.19	-1.86	110,113,113,115	1
2	FES	A	3002	4/4	0.98	0.12	-2.14	89,90,90,92	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.